

## SEQUENCE LISTING

<110> Presnell, Scott R.  
Burkhead, Steven K.  
Powder, Sarah L.

<120> Human Cytokine Receptor

<130> 99-50

<160> 12

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2255

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (154)...(2229)

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cctcaggcct gggtgccacc tggcacctag aag atg cct gtg ccc tgg ttc ttg 174  
Met Pro Val Pro Trp Phe Leu  
1 5

ctg tcc ttg gca ctg ggc cga agc cca gtg gtc ctt tct ctg gag agg 222  
Leu Ser Leu Ala Leu Gly Arg Ser Pro Val Val Leu Ser Leu Glu Arg  
10 15 20

ctt gtg ggg cct cag gac gct acc cac tgc tct ccg ggc ctc tcc tgc 270  
Leu Val Gly Pro Gln Asp Ala Thr His Cys Ser Pro Gly Leu Ser Cys  
25 30 35

cgc ctc tgg gac agt gac ata ctc tgc ctg cct ggg gac atc gtg cct 318  
Arg Leu Trp Asp Ser Asp Ile Leu Cys Leu Pro Gly Asp Ile Val Pro  
40 45 50 55

Sub A1

A

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235 240 245	
aac cac aca gac ctg gtt ccc tgc ctc tgt att cag gtg tgg cct ctg	942
Asn His Thr Asp Leu Val Pro Cys Leu Cys Ile Gln Val Trp Pro Leu	
250 255 260	
gaa cct gac tcc gtt agg acg aac atc tgc ccc ttc agg gag gac ccc	990
Glu Pro Asp Ser Val Arg Thr Asn Ile Cys Pro Phe Arg Glu Asp Pro	
265 270 275	
cgc gca cac cag aac ctc tgg caa gcc gcc cga ctg cga ctg ctg acc	1038
Arg Ala His Gln Asn Leu Trp Gln Ala Ala Arg Leu Arg Leu Leu Thr	
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Leu Gln Ser Trp Leu Leu Asp Ala Pro Cys Ser Leu Pro Ala Glu Ala	
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Pro Pro Leu Ser Trp Glu Asn Val Thr Val Asp Lys Val Leu Glu Phe	
330 335 340	
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Pro Leu Leu Lys Gly His Pro Asn Leu Cys Val Gln Val Asn Ser Ser	
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Glu Lys Leu Gln Leu Gln Glu Cys Leu Trp Ala Asp Ser Leu Gly Pro	
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Leu Lys Asp Asp Val Leu Leu Leu Glu Thr Arg Gly Pro Gln Asp Asn	
380 385 390	
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Arg Ser Leu Cys Ala Leu Glu Pro Ser Gly Cys Thr Ser Leu Pro Ser	
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Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile His Lys Arg Trp Ala Leu	
440 445 450 455	
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Val Trp Leu Ala Cys Leu Leu Phe Ala Ala Ala Leu Ser Leu Ile Leu	
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Leu Trp Ser Arg Arg Glu Leu Ser Ala Gln Gly Pro Val Ala Trp Phe	
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His Ala Gln Arg Arg Gln Thr Leu Gln Glu Gly Gly Val Val Val Leu	
540 545 550	
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Leu Phe Ser Pro Gly Ala Val Ala Leu Cys Ser Glu Trp Leu Gln Asp	
555 560 565	

Met Pro Val Pro Trp Phe Leu Leu Ser Leu Ala Leu Gly Arg Ser Pro  
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Val Val Leu Ser Leu Glu Arg Leu Val Gly Pro Gln Asp Ala Thr His  
 20 25 30  
 Cys Ser Pro Gly Leu Ser Cys Arg Leu Trp Asp Ser Asp Ile Leu Cys  
 35 40 45  
 Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr  
 50 55 60  
 His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys  
 65 70 75 80  
 Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp  
 85 90 95  
 Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Ser Gly  
 100 105 110  
 Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser  
 115 120 125  
 Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val  
 130 135 140  
 Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr  
 145 150 155 160  
 Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr  
 165 170 175  
 Thr Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro  
 180 185 190  
 Ala Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu  
 195 200 205  
 Val Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp  
 210 215 220  
 Asn Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr  
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 Gly Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu  
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 Cys Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile  
 260 265 270  
 Cys Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala  
 275 280 285  
 Ala Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro  
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 Cys Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly  
 305 310 315 320  
 Asp Pro Cys Gln Pro Leu Val Pro Pro Leu Ser Trp Glu Asn Val Thr  
 325 330 335  
 Val Asp Lys Val Leu Glu Phe Pro Leu Leu Lys Gly His Pro Asn Leu  
 340 345 350

Cys Val Gln Val Asn Ser Ser Glu Lys Leu Gln Leu Gln Glu Cys Leu  
 355 360 365  
 Trp Ala Asp Ser Leu Gly Pro Leu Lys Asp Asp Val Leu Leu Leu Glu  
 370 375 380  
 Thr Arg Gly Pro Gln Asp Asn Arg Ser Leu Cys Ala Leu Glu Pro Ser  
 385 390 395 400  
 Gly Cys Thr Ser Leu Pro Ser Lys Ala Ser Thr Arg Ala Ala Arg Leu  
 405 410 415  
 Gly Glu Tyr Leu Leu Gln Asp Leu Gln Ser Gly Gln Cys Leu Gln Leu  
 420 425 430  
 Trp Asp Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr  
 435 440 445  
 Ile His Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala  
 450 455 460  
 Ala Ala Leu Ser Leu Ile Leu Leu Lys Lys Asp His Ala Lys Ala  
 465 470 475 480  
 Ala Ala Arg Gly Arg Ala Ala Leu Leu Leu Tyr Ser Ala Asp Asp Ser  
 485 490 495  
 Gly Phe Glu Arg Leu Val Gly Ala Leu Ala Ser Ala Leu Cys Gln Leu  
 500 505 510  
 Pro Leu Arg Val Ala Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala  
 515 520 525  
 Gln Gly Pro Val Ala Trp Phe His Ala Gln Arg Arg Gln Thr Leu Gln  
 530 535 540  
 Glu Gly Gly Val Val Val Leu Leu Phe Ser Pro Gly Ala Val Ala Leu  
 545 550 555 560  
 Cys Ser Glu Trp Leu Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly  
 565 570 575  
 Pro His Asp Ala Phe Arg Ala Ser Leu Ser Cys Val Leu Pro Asp Phe  
 580 585 590  
 Leu Gln Gly Arg Ala Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg  
 595 600 605  
 Leu Leu His Pro Asp Ala Val Pro Ala Leu Phe Arg Thr Val Pro Val  
 610 615 620  
 Phe Thr Leu Pro Ser Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln  
 625 630 635 640  
 Pro Arg Ala Pro Arg Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val  
 645 650 655  
 Ser Arg Ala Leu Gln Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly  
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Gly Asp Gly Thr  
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<210> 3

<211> 2076

<212> DNA

<213> Artificial Sequence

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sequence of SEQ ID NO:2.

<221> variation

<222> (1)...(2076)

<223> N is any nucleotide

<221> misc\_feature

<222> (1)...(2076)

<223> n = A,T,C or G

<400> 3

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ytngcncna	cncayytnc	racngarytn	gtnytnmgnt	gycaraarga	racngaytgy	240
gayytnygy	tnmgngtngc	ngtncayytn	gcngtncayg	gncaytggga	rgarccngar	300
gaygargara	arttyggngg	ngcngcngay	wsngngtng	argarccnmg	naaygcwnsn	360
ytncargcnc	argtngtnyt	nwsnttycar	gcntayccna	cngcnmgntg	ygtnytnytn	420
gargtncarg	tnccngcngc	nytngtncar	ttyggncarw	sngtnggnws	ngtngtntay	480
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taygaraarg	arytnaayca	yacncarcar	ytncngcny	tnccntggyt	naaygtnwsn	600
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ggncncncara	thathacnyt	naaycayacn	gayytngtnc	cntggytntg	yathcargtn	780
tggccnytn	arccngayws	ngtnmgnacn	aayathgtgc	cnttymnga	rgayccnmgn	840
gcncaycara	ayytnyggca	rgcngcnmgn	ytngmnytny	tnacnytnca	rwsntggytn	900
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ytncargayy	tnarwsngg	ncartgyytn	carytnyggg	aygaygayt	ngngcnytn	1320



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ttymgngcnw	snytnwsntg	ygtnytnccn	gayttyytn	arggnmgngc	nccnggnwsn	1800
taygtnggng	cntgyttyga	ymgnytnytn	cayccngayg	cngtnccngc	nytnnttymgn	1860
acngtnccng	tnntyacny	nccnwsncar	ytnccngayt	tyytnggngc	nytnccarcar	1920
ccnmgngcnc	cnmgngwsngg	nmgnytnncar	garmgngcng	arcargtnws	nmgngcnytn	1980
carccngcny	tngaywsnta	ytycayccn	ccnggnacnc	cngcncngg	nmgnggngtn	2040
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&lt;210&gt; 4

&lt;211&gt; 1753

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (2)...(1726)

&lt;400&gt; 4

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cag	gcc	tac	cct	act	gcc	cgc	tgc	gtc	ctg	ctg	gag	gtg	caa	gtg	cct	97
Gln	Ala	Tyr	Pro	Thr	Ala	Arg	Cys	Val	Leu	Leu	Glu	Val	Gln	Val	Pro	
			20					25					30			

gct	gcc	ctt	gtg	cag	ttt	ggt	cag	tct	gtg	ggc	tct	gtg	gta	tat	gac	145
Ala	Ala	Leu	Val	Gln	Phe	Gly	Gln	Ser	Val	Gly	Ser	Val	Val	Tyr	Asp	
		35					40					45				

tgc	ttc	gag	gct	gcc	cta	ggg	agt	gag	gta	cga	atc	tgg	tcc	tat	act	193
Cys	Phe	Glu	Ala	Ala	Leu	Gly	Ser	Glu	Val	Arg	Ile	Trp	Ser	Tyr	Thr	
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cag	ccc	agg	tac	gag	aag	gaa	ctc	aac	cac	aca	cag	cag	ctg	cct	gcc	241
Gln	Pro	Arg	Tyr	Glu	Lys	Glu	Leu	Asn	His	Thr	Gln	Gln	Leu	Pro	Ala	
	65					70				75					80	

ctg ccc tgg ctc aac gtg tca gca gat ggt gac aac gtg cat ctg gtt Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu Val 85 90 95	289
ctg aat gtc tct gag gag cag cac ttc ggc ctc tcc ctg tac tgg aat Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp Asn 100 105 110	337
cag gtc cag ggc ccc cca aaa ccc cgg tgg cac aaa aac ctg act gga Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr Gly 115 120 125	385
ccg cag atc att acc ttg aac cac aca gac ctg gtt ccc tgc ctc tgt Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu Cys 130 135 140	433
att cag gtg tgg cct ctg gaa cct gac tcc gtt agg acg aac atc tgc Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile Cys 145 150 155 160	481
ccc ttc agg gag gac ccc cgc gca cac cag aac ctc tgg caa gcc gcc Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala Ala 165 170 175	529
cga ctg cga ctg ctg acc ctg cag agc tgg ctg ctg gac gca ccg tgc Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro Cys 180 185 190	577
tcg ctg ccc gca gaa gcg gca ctg tgc tgg cgg gct ccg ggt ggg gac Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly Asp 195 200 205	625
ccc tgc cag cca ctg gtc cca ccg ctt tcc tgg gag aac gtc act gtg Pro Cys Gln Pro Leu Val Pro Pro Leu Ser Trp Glu Asn Val Thr Val 210 215 220	673
gac gtg aac agc tcg gag aag ctg cag ctg cag gag tgc ttg tgg gct Asp Val Asn Ser Ser Glu Lys Leu Gln Leu Gln Glu Cys Leu Trp Ala 225 230 235 240	721
gac tcc ctg ggg cct ctc aaa gac gat gtg cta ctg ttg gag aca cga	769

Asp Ser Leu Gly Pro Leu Lys Asp Asp Val Leu Leu Leu Glu Thr Arg	
245 250 255	
ggc ccc cag gac aac aga tcc ctc tgt gcc ttg gaa ccc agt ggc tgt	817
Gly Pro Gln Asp Asn Arg Ser Leu Cys Ala Leu Glu Pro Ser Gly Cys	
260 265 270	
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Thr Ser Leu Pro Ser Lys Ala Ser Thr Arg Ala Ala Arg Leu Gly Glu	
275 280 285	
tac tta cta caa gac ctg cag tca ggc cag tgt ctg cag cta tgg gac	913
Tyr Leu Leu Gln Asp Leu Gln Ser Gly Gln Cys Leu Gln Leu Trp Asp	
290 295 300	
gat gac ttg gga gcg cta tgg gcc tgc ccc atg gac aaa tac atc cac	961
Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile His	
305 310 315 320	
aag cgc tgg gcc ctc gtg tgg ctg gcc tgc cta ctc ttt gcc gct gcg	1009
Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala Ala Ala	
325 330 335	
ctt tcc ctc atc ctc ctt ctc aaa aag gat cac gcg aaa ggg tgg ctg	1057
Leu Ser Leu Ile Leu Leu Leu Lys Lys Asp His Ala Lys Gly Trp Leu	
340 345 350	
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Arg Leu Leu Lys Gln Asp Val Arg Ser Gly Ala Ala Ala Arg Gly Arg	
355 360 365	
gcg gct ctg ctc ctc tac tca gcc gat gac tcg ggt ttc gag cgc ctg	1153
Ala Ala Leu Leu Leu Tyr Ser Ala Asp Asp Ser Gly Phe Glu Arg Leu	
370 375 380	
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Val Gly Ala Leu Ala Ser Ala Leu Cys Gln Leu Pro Leu Arg Val Ala	
385 390 395 400	
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Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala Gln Gly Pro Val Ala	
405 410 415	

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Trp Phe His Ala Gln Arg Arg Gln Thr Leu Gln Glu Gly Gly Val Val	
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gtc ttg ctc ttc tct ccc ggt gcg gtg gcg ctg tgc agc gag tgg cta	1345
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435 440 445	
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Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly Pro His Asp Ala Phe	
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Arg Ala Ser Leu Ser Cys Val Leu Pro Asp Phe Leu Gln Gly Arg Ala	
465 470 475 480	
ccc ggc agc tac gtg ggg gcc tgc ttc gac agg ctg ctc cac ccg gac	1489
Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg Leu Leu His Pro Asp	
485 490 495	
gcc gta ccc gcc ctt ttc cgc acc gtg ccc gtc ttc aca ctg ccc tcc	1537
Ala Val Pro Ala Leu Phe Arg Thr Val Pro Val Phe Thr Leu Pro Ser	
500 505 510	
caa ctg cca gac ttc ctg ggg gcc ctg cag cag cct cgc gcc ccg cgt	1585
Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln Pro Arg Ala Pro Arg	
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tcc ggg cgg ctc caa gag aga gcg gag caa gtg tcc cgg gcc ctt cag	1633
Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val Ser Arg Ala Leu Gln	
530 535 540	
cca gcc ctg gat agc tac ttc cat ccc ccg ggg act ccc gcg ccg gga	1681
Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly Thr Pro Ala Pro Gly	
545 550 555 560	
cgc ggg gtg gga cca ggg gcg gga cct ggg gcg ggg gac ggg act	1726
Arg Gly Val Gly Pro Gly Ala Gly Pro Gly Ala Gly Asp Gly Thr	
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taaataaagg cagacgctgt ttttcta	1753

<211> 575  
 <212> PRT  
 <213> Homo sapiens

<400> 5

Glu	Glu	Pro	Arg	Asn	Ala	Ser	Leu	Gln	Ala	Gln	Val	Val	Leu	Ser	Phe
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			20					25					30		
Ala	Ala	Leu	Val	Gln	Phe	Gly	Gln	Ser	Val	Gly	Ser	Val	Val	Tyr	Asp
		35					40					45			
Cys	Phe	Glu	Ala	Ala	Leu	Gly	Ser	Glu	Val	Arg	Ile	Trp	Ser	Tyr	Thr
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Gln	Pro	Arg	Tyr	Glu	Lys	Glu	Leu	Asn	His	Thr	Gln	Gln	Leu	Pro	Ala
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Gly	Pro	Gln	Asp	Asn	Arg	Ser	Leu	Cys	Ala	Leu	Glu	Pro	Ser	Gly	Cys
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Thr	Ser	Leu	Pro	Ser	Lys	Ala	Ser	Thr	Arg	Ala	Ala	Arg	Leu	Gly	Glu
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Tyr	Leu	Leu	Gln	Asp	Leu	Gln	Ser	Gly	Gln	Cys	Leu	Gln	Leu	Trp	Asp
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Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly Pro His Asp Ala Phe
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Leu	Pro	Gly	Asp	Ile	Val	Pro	Ala	Pro	Gly	Pro	Val	Leu	Ala	Pro	Thr
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His	Leu	Gln	Thr	Glu	Leu	Val	Leu	Arg	Cys	Gln	Lys	Glu	Thr	Asp	Cys
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Asp	Leu	Cys	Leu	Arg	Val	Ala	Val	His	Leu	Ala	Val	His	Gly	His	Trp
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Glu	Glu	Pro	Glu	Asp	Glu	Glu	Lys	Phe	Gly	Gly	Ala	Ala	Asp	Ser	Gly
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Asp	Cys	Phe	Glu	Ala	Ala	Leu	Gly	Ser	Glu	Val	Arg	Ile	Trp	Ser	Tyr
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Val	Leu	Asn	Val	Ser	Glu	Glu	Gln	His	Phe	Gly	Leu	Ser	Leu	Tyr	Trp
	210					215					220				
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 Asp Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile  
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 His Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala Ala  
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 Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr  
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 His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys  
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 Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp  
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 Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Ser Gly  
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 Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val  
 130 135 140  
 Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr  
 145 150 155 160  
 Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr  
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 Thr Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro  
 180 185 190  
 Ala Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu  
 195 200 205  
 Val Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp  
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 Asn Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr  
 225 230 235 240  
 Gly Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu  
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 260 265 270

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 Asp Pro Cys Gln Pro Leu Val Pro Pro Leu Ser Trp Glu Asn Val Thr  
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Sub A1  
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 35 40 45  
 Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr  
 50 55 60  
 His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys  
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 Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp  
 85 90 95  
 Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Ser Gly  
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 Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser  
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SubA  
Cont.

Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr  
 145 150 155 160  
 Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr  
 165 170 175  
 Thr Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro  
 180 185 190  
 Ala Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu  
 195 200 205  
 Val Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp  
 210 215 220  
 Asn Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr  
 225 230 235 240  
 Gly Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu  
 245 250 255  
 Cys Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile  
 260 265 270  
 Cys Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala  
 275 280 285  
 Ala Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro  
 290 295 300  
 Cys Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly  
 305 310 315 320  
 Asp Pro Cys Gln Pro Leu Val Pro Pro Leu Ser Trp Glu Asn Val Thr  
 325 330 335  
 Val Asp Val Asn Ser Ser Glu Lys Leu Gln Leu Gln Glu Cys Leu Trp  
 340 345 350  
 Ala Asp Ser Leu Gly Pro Leu Lys Asp Asp Val Leu Leu Glu Thr  
 355 360 365  
 Arg Gly Pro Gln Asp Asn Arg Ser Leu Cys Ala Leu Glu Pro Ser Gly  
 370 375 380  
 Cys Thr Ser Leu Pro Ser Lys Ala Ser Thr Arg Ala Ala Arg Leu Gly  
 385 390 395 400  
 Glu Tyr Leu Leu Gln Asp Leu Gln Ser Gly Gln Cys Leu Gln Leu Trp  
 405 410 415  
 Asp Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile  
 420 425 430  
 His Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala Ala  
 435 440 445  
 Ala Leu Ser Leu Ile Leu Leu Leu Lys Lys Asp His Ala Lys Ala Ala  
 450 455 460  
 Ala Arg Gly Arg Ala Ala Leu Leu Leu Tyr Ser Ala Asp Asp Ser Gly  
 465 470 475 480

Sub A1  
cont.

145 150 155 160  
 165 170 175  
 180 185 190  
 195 200 205  
 210 215 220  
 225 230 235 240  
 245 250 255  
 260 265 270  
 275 280 285  
 290 295 300  
 305 310 315 320  
 325 330 335  
 340 345 350  
 355 360 365  
 370 375 380  
 385 390 395 400  
 405 410 415  
 420 425 430  
 435 440 445  
 450 455 460  
 465 470 475 480

Sub A  
cont.